

The figure displays a sequence logo for a protein sequence spanning positions 810 to 990. The y-axis represents the frequency of each amino acid at each position, with a color scale ranging from black (0) to magenta (~0.9). The x-axis represents the positions. The sequence is highly conserved, with most positions showing a single dominant amino acid. Key features include a large cluster of hydrophobic residues (black/red) between positions 810-850, followed by a series of polar and charged residues (green/blue/purple) extending to position 990. A notable insertion of a long stretch of hydrophobic residues (black/red) is present around position 900.

1600 1410 1420 1430 1440 1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550 1560 1570 1580 1590

113r_PKA_ca VNDIKNFKPATTDVIAIYORKVEAPFIFKFKPGD - TSNFDDYEEEIRVX - INEKCGKEFTF
1jlu_AMPK VNDIKNFKPATTDVIAIYORKVEAPFIFKFKPGD - TSNFDDYEEEIRVX - INEKCGKEFTF
39978255.Y AAEIKRHPERTTQWALLRL-TPPITPDG - PDGNFRTLKDSQSVDIGG- ATRKVADDDEFSAFSVTILHYGDDK-
32415513.Y ASDIKQPFPEPTTQWALLRM-KPPIPVNQGRG - IDTILNFRNKESESVDISGSRQAGLKGEPLESGM - VTFGENAVDFEEENSVTILHHIDDEEYHSDAYEKR-
19113518.Y AADVKLHFPEFKVNWALLRTE-EPPIIPKLAPIDEKGNNISHLKEKSLSLDITHSPQNTQTVEVPLSN - LSGADHGDDFESFNSVTWHHEWD-
19113518.Y AADVIKRPFFFKVNWALLRTE-EPPIIPKLAPIDEKGNNISHLKEKSLSLDITHSPQNTQTVEVPLSN - LSGADHGDDFESFNSVTWHHEWD-
10383810.Y AADVIKRPFFFKVNWALLRTE-DPPIIPALNONGCELPPILSCKNHPK - RNSVSBQETKMPCEKVA - NDDEIDEADEPHFDENSMSLTKDHNLITYSENTYTGKILYKATCTR-RHNSHRSFKDIIPEL
6324375.Y AADVKKHFPEFKVNWALLRTE-EPPIIPVLSLEDGYDFAKLSSNNKRTQTSQDSHKHDLQEKNMFEEERVE - YDDEVSEDDFPHDFNSMSLMEQDNNSMIYGNJNSYGKIAYPNSNRSRNS-HRTFFFKR
AK065447 VAPMR - PCL -
AK066816 ANEIKKRPFFGICINWALLRCA-PKLEIPLFKEDDM - EKKGLVLTNNR - TDMP-
15231245.P ANEVKQHFFGICINWALLRCNPELETPIFGSEAE - NGEKVVDPFL - EDLQTNF
83522140 ANDIKQHFFGICINWALLRCMSEPELDVPLKLIGKE - TQKAKPDED - VPFLNDF
AK067128 ANDIKQHFFGICINWALLRCMSEPELDVPLKLIGKE - TQKAKPDED - VPFLNDF
30697007.P ANEIKKRPFFGICINWALLRCMSPPLDAPLSIIEKD - PNAKDIKWEDDGVL - VNSTDLDIDDF
30697010.P ANEIKKRPFFGICINWALLRCMSPPLDAPLSIIEKD - PNAKDIKWEDDGVL - VNSTDLDIDDF
30697012.P ANEIKKRPFFGICINWALLRCMSPPLDAPLSIIEKD - PNAKDIKWEDDGVL - VNSTDLDIDDF
30450014
36050006 ADEVRAFFFGQVNDLIGELSPRPPYIPPPADIAA - CEGFSVVEYFNKLIHE - PSPE - PEEEEEFLPBP
18403402.P AAEIKRHPFFGICINWALLRCA-APPETPFLPFL - VTEESFGIGKEYFEKLKT - PPLFL - PHCESENN-FVDF
15232374.P AAEIKRHPFFGICINWALLRCA-APPETPFLPFL - VGGFDIREHFKRDLRTTFS - SAPPSPLRSPPHVCRKND-FIIF
15230825.P VEEIKRHPFFGICINWALLRCA-APPETPFLPFL - TDVNWKMDVENVIVQEIFAARQEREKQSGDNNKNAWMKIDNTSGEWVKGLNNNDLESNNFLV - CEHNGNFIWF
15235548.P VECIKKHFDFKGLDVLVLIKVSPPYIPAPEN - YEISKIDIVEKFVBEIFTK -
83523772.P ARGKIKRHPFFGICINWALLRCA-APPETPFLPFL - EAGEFVLDVKEVNVNEFAAND - GGAAAGCVKEKPSPAGGTILAVGDGEQRDRDPEKEGFSFF -
52520008 AAVIKRHPFFGICINWALLRCA-TPPVYPLPFL - FSVATAATANAAAANADM - SYDCCSDEGTVFVY
30692190.P ATAVKRPFFGICINWALLRCA-APPETPFLPFL - FRKLELL - DDCIFETHVDFY
AK107126 AAEIKRHPFFGICINWALLRCA-APPETPFLPFL - TLTTAKKKVGKCL - EFRNLGDDIEFDF
AK065005 AAEIKRHPFFGICINWALLRCA-APPETPFLPFL - SLTTARKKKEGKCL - EFRNLGDDIEFDF
30693721.P SVEIKRHPFFGICINWALLRCA-IPPDLPDYFYEGGG - PEAADSPGGSNNRYL - ECKAIGDHLFEDF
30693719.P SVEIKRHPFFGICINWALLRCA-IPPDLPDYFYEGGG - PEAADSPGGSNNRYL - ECKAIGDHLFEDF
15227639.P AAEIKRHPFFGICINWALLRCA-IPPDLPDYFYEGGG - ATAEATSEEG_NNRYL - ECKAIGDHLFEDF
15242814.P AAEIKRHPFFGICINWALLRCA-IPPDLPDYFYEGGG - VPNPNECKSNYL - DCKAVGEHLEFDF
AK101944 AAEIKRHPFFGICINWALLRCA-TPPDVPVR - VEAELPAKYG - VAEPVASGGGGKRVVG - AEVRSGGGKYLDFF
83020012 AAEIKRHPFFGICINWALLRCA-TPPDVPVR - VEAELPVKYG - VEAAGIS - NSKRMVG - ADMXPSGGKFLLFDF
30689844.P AAEIKRHPFFGICINWALLRCA-TPPDVPVR-METEPFPXYG - P1DVPFGSNSKRMGP - PAVSAAAADTKSGGFLLFDF
15241076.P AAEIKRHPFFGICINWALLRCA-SPPBTPK - VDLEA - LNPTTIVAAASS - SVRSDQSNYLFDF
15236802.P AAEIKRHPFFGICINWALLRCA-SPPBTPK - WDYES - APATP - AAASTST - SVKSDQSNYLFDF
15238798.P AAEIKRHPFFGICINWALLRCA-TPPBPVPE - VELEKGA - V - SVAEAPSSQTAAGLVL - NAQKGSDNYLFDF
AK065888 AAEIKRHPFFGICINWALLRCA-SPPBTPK - VEIER - PKLPPGSTGTTDVS - APQPKGSDYLFDF
AK100261 AAEIKRHPFFGICINWALLRCA-SPPBTPK - VEIER - PFKQPVSTSEPAAPSD - AAQKSSDQSNYLFDF
AK100536 AAEIKRHPFFGICINWALLRCA-SPPBTPK - VELDC - R-KQVPSSTNGKVNAPAS - NQKGSDNYLFDF
AK103656 AAEIKRHPFFGICINWALLRCA-SPPBTPK - VELER - PKPKPAT - EKVAPA - NQKGSDNYLFDF
AK070835 AAEIKRHPFFGICINWALLRCA-TPPDTPK - VEI - PRSVASTSKATTIA - EKGSDNYLFDF
15242554.P AAEIKRHPFFGICINWALLRCA-TPPDTPK - IDLSILN - ETIKSSVQOOQVHNSK - QSDSSSGFYLDF
15232201.P AAEIKRHPFFGICINWALLRCA-TPPDTPK - VKPMD - QAHSVRHGFSGQGHGVG - YDKPTTVKPSGNYLFDF
15219253.P AAEIKRHPFFGICINWALLRCA-TPPDTPK - WDFSCYVKE - KESLPPAATEKKSK - MFDEANKSGSDPYIVDF
15219322.P AAEIKRHPFFGICINWALLRCA-TPPDTPK - WDFSCYASKD - KESMAAVDGGKKNNNAG - GGCSTGGDNKPNDCNDPYIDF
15230566.P AAEIKRHPFFGICINWALLRCA-APPETPFL - VDLGYAAAR - GKTKHGGGDHCNSMK - PEFLVACAAGPTDIAHDF
AK107045 AAEIKRHPFFGICINWALLRCA-TPPDVPVR - VFRCQYAAAATTPKDKPPENAAAAAAPA - AADGGGAANSSTGES-YIDF
AK069983 AAEIKRHPFFGICINWALLRCA-APPETPFL - VDFSQFGVRE - KPAAPATKVAKPA - ASD - SSSGD
83511682 AAEIKRHPFFGICINWALLRCA-MPPVLPPEADAAAADC - PLARATQGGGT - KSAAGGKASSPRDDPSVYF
15225776.P SHIEIKRHPFFGICINWALLRCA-KPPPVPEKEETSHKTKGDNRS - VNYYLPPRFMMRSRKERN - EPYHVS - NYEDF
AK101660 SAEVKRPFFGICINWALLRCA-APPETPFL - VMTMSKKERQ - EPYNYR - ENFDF
AK106290 RADVKSHFFKSLNALLRSS - RPPVVPAGAGAFLHRSQ - SCKAAPTPPPPFTT - KPNAT - ARDF
74030009 RADVKSHFFKSLNALLRSS - APPVVP - PFAVAAAACS - KAADV - ODFDF
15226800.P AAEVKRPFFGICINWALLRCA-TPPDTPK - SSVKKPMKSATFSG - RSSNPK - AAEDF
15231840.P AODIKRHPFFGICINWALLRCA-KPPEE - VRGLVIKKSTRPHAS - HVIAVSPRRKSFLWRA - LSYLLRGKSSS-GGSKNQSNNSYHIVGKSYASRKRV
15220907.P AODIKRHPFFGICINWALLRCA-KPPEE - IGLVKK - TKAAG - HVIATAVTPRNKWLWVA - LSHLLRSKSLSKSSKIQQNNNYHIVVGKKL
71430020 AAEIKRHPFFGICINWALLRCA-APPVPDKDSAAGAGDKKAKLG - SWNSMGKKRSFGRKS - NYEERQGVFRKLMWSQDSRSKAKINKV
1muo_AUR1 EVIIFPPTTANSKSK-SNCQNKESASKQS -
1omw_GPRK2 POFIFPPTTANSKSK-SNCQNKESASKQS -

113r_PKACa 1610 1620 1630 1640
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AK067128
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